

## SEQUENCE LISTING

<110> Kunkel, Andreas  
 Veen, Markus  
 Lang, Christine

<120> Method for producing ergosta-5,7-dienol and/or biosynthetic  
 intermediate and/or secondary products thereof in transgenic  
 organisms

<130> 12810-00126-US

<150> PCT/EP2004/002582

<151> 2004-03-12

<150> DE 103 12 314.8

<151> 2003-03-19

<160> 14

<170> PatentIn version 3.3

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<213> Saccharomyces cerevisiae

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Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser  
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Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala  
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Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu Glu Gly  
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Phe	Val	Phe	Pro	Asn	Leu	Pro	Leu	Glu	His	Tyr	Arg	Lys	Arg	Asp	His	
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Gln	Gln	Glu	Leu	Tyr	Glu	Glu	Gln	Met	Arg	Val	Leu	Asp	Gly	Gly	Lys	
			340					345					350			
aag	gaa	ttg	acc	tac	gat	tta	tta	caa	gaa	atg	cca	ttg	ttg	aac	caa	1104
Lys	Glu	Leu	Thr	Tyr	Asp	Leu	Leu	Gln	Glu	Met	Pro	Leu	Leu	Asn	Gln	
		355					360					365				
act	att	aag	gaa	act	cta	aga	atg	cac	cat	cca	ttg	cac	tct	ttg	ttc	1152
Thr	Ile	Lys	Glu	Thr	Leu	Arg	Met	His	His	Pro	Leu	His	Ser	Leu	Phe	
	370					375					380					
cgt	aag	gtt	atg	aaa	gat	atg	cac	gtt	cca	aac	act	tct	tat	gtc	atc	1200
Arg	Lys	Val	Met	Lys	Asp	Met	His	Val	Pro	Asn	Thr	Ser	Tyr	Val	Ile	
385					390					395					400	
cca	gca	ggg	tat	cac	gtt	ttg	gtt	tct	cca	ggg	tac	act	cat	tta	aga	1248
Pro	Ala	Gly	Tyr	His	Val	Leu	Val	Ser	Pro	Gly	Tyr	Thr	His	Leu	Arg	
				405					410					415		
gac	gaa	tac	ttc	cct	aat	gct	cac	caa	ttc	aac	att	cac	cgt	tgg	aac	1296
Asp	Glu	Tyr	Phe	Pro	Asn	Ala	His	Gln	Phe	Asn	Ile	His	Arg	Trp	Asn	
			420					425					430			
aaa	gat	tct	gcc	tcc	tct	tat	tcc	gtc	ggg	gaa	gaa	gtc	gat	tac	ggg	1344
Lys	Asp	Ser	Ala	Ser	Ser	Tyr	Ser	Val	Gly	Glu	Glu	Val	Asp	Tyr	Gly	
		435					440					445				
ttc	ggg	gcc	att	tct	aag	ggg	gtc	agc	tct	cca	tac	tta	cct	ttc	ggg	1392
Phe	Gly	Ala	Ile	Ser	Lys	Gly	Val	Ser	Ser	Pro	Tyr	Leu	Pro	Phe	Gly	
	450					455					460					
ggg	ggg	aga	cac	aga	tgt	atc	ggg	gaa	cac	ttt	gct	tac	tgt	cag	cta	1440
Gly	Gly	Arg	His	Arg	Cys	Ile	Gly	Glu	His	Phe	Ala	Tyr	Cys	Gln	Leu	
465					470					475					480	
ggg	gtt	cta	atg	tcc	att	ttt	atc	aga	aca	tta	aaa	tgg	cat	tac	cca	1488
Gly	Val	Leu	Met	Ser	Ile	Phe	Ile	Arg	Thr	Leu	Lys	Trp	His	Tyr	Pro	
				485					490					495		
gag	ggg	aag	acc	gtt	cca	cct	cct	gac	ttt	aca	tct	atg	gtt	act	ctt	1536
Glu	Gly	Lys	Thr	Val	Pro	Pro	Pro	Asp	Phe	Thr	Ser	Met	Val	Thr	Leu	

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                    500                    505                    510
cca acc ggt cca gcc aag atc atc tgg gaa aag aga aat cca gaa caa      1584
Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln
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aag atc taa
Lys Ile
    530

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<212> PRT
<213> Saccharomyces cerevisiae

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Ile Gly Leu Ser His Phe Leu Ala Leu Pro Leu Ala Gln Arg Ile Ser
                    20                    25                    30

Leu Ile Ile Ile Ile Pro Phe Ile Tyr Asn Ile Val Trp Gln Leu Leu
    35                    40                    45

Tyr Ser Leu Arg Lys Asp Arg Pro Pro Leu Val Phe Tyr Trp Ile Pro
    50                    55                    60

Trp Val Gly Ser Ala Val Val Tyr Gly Met Lys Pro Tyr Glu Phe Phe
65                    70                    75                    80

Glu Glu Cys Gln Lys Lys Tyr Gly Asp Ile Phe Ser Phe Val Leu Leu
                    85                    90                    95

Gly Arg Val Met Thr Val Tyr Leu Gly Pro Lys Gly His Glu Phe Val
                    100                    105                    110

Phe Asn Ala Lys Leu Ala Asp Val Ser Ala Glu Ala Ala Tyr Ala His
    115                    120                    125

Leu Thr Thr Pro Val Phe Gly Lys Gly Val Ile Tyr Asp Cys Pro Asn
    130                    135                    140

Ser Arg Leu Met Glu Gln Lys Lys Phe Val Lys Gly Ala Leu Thr Lys
145                    150                    155                    160

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Glu Ala Phe Lys Ser Tyr Val Pro Leu Ile Ala Glu Glu Val Tyr Lys  
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Tyr Phe Arg Asp Ser Lys Asn Phe Arg Leu Asn Glu Arg Thr Thr Gly  
 180 185 190

Thr Ile Asp Val Met Val Thr Gln Pro Glu Met Thr Ile Phe Thr Ala  
 195 200 205

Ser Arg Ser Leu Leu Gly Lys Glu Met Arg Ala Lys Leu Asp Thr Asp  
 210 215 220

Phe Ala Tyr Leu Tyr Ser Asp Leu Asp Lys Gly Phe Thr Pro Ile Asn  
 225 230 235 240

Phe Val Phe Pro Asn Leu Pro Leu Glu His Tyr Arg Lys Arg Asp His  
 245 250 255

Ala Gln Lys Ala Ile Ser Gly Thr Tyr Met Ser Leu Ile Lys Glu Arg  
 260 265 270

Arg Lys Asn Asn Asp Ile Gln Asp Arg Asp Leu Ile Asp Ser Leu Met  
 275 280 285

Lys Asn Ser Thr Tyr Lys Asp Gly Val Lys Met Thr Asp Gln Glu Ile  
 290 295 300

Ala Asn Leu Leu Ile Gly Val Leu Met Gly Gly Gln His Thr Ser Ala  
 305 310 315 320

Ala Thr Ser Ala Trp Ile Leu Leu His Leu Ala Glu Arg Pro Asp Val  
 325 330 335

Gln Gln Glu Leu Tyr Glu Glu Gln Met Arg Val Leu Asp Gly Gly Lys  
 340 345 350

Lys Glu Leu Thr Tyr Asp Leu Leu Gln Glu Met Pro Leu Leu Asn Gln  
 355 360 365

Thr Ile Lys Glu Thr Leu Arg Met His His Pro Leu His Ser Leu Phe  
 370 375 380

Arg Lys Val Met Lys Asp Met His Val Pro Asn Thr Ser Tyr Val Ile  
385 390 395 400

Pro Ala Gly Tyr His Val Leu Val Ser Pro Gly Tyr Thr His Leu Arg  
405 410 415

Asp Glu Tyr Phe Pro Asn Ala His Gln Phe Asn Ile His Arg Trp Asn  
420 425 430

Lys Asp Ser Ala Ser Ser Tyr Ser Val Gly Glu Glu Val Asp Tyr Gly  
435 440 445

Phe Gly Ala Ile Ser Lys Gly Val Ser Ser Pro Tyr Leu Pro Phe Gly  
450 455 460

Gly Gly Arg His Arg Cys Ile Gly Glu His Phe Ala Tyr Cys Gln Leu  
465 470 475 480

Gly Val Leu Met Ser Ile Phe Ile Arg Thr Leu Lys Trp His Tyr Pro  
485 490 495

Glu Gly Lys Thr Val Pro Pro Pro Asp Phe Thr Ser Met Val Thr Leu  
500 505 510

Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln  
515 520 525

Lys Ile  
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<211> 1491  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
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att acc tac gat gcg att gtc atc ggt gct ggt gtt atc ggt cca tgt 96  
Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys  
20 25 30



gtt gct act ggt cta gca aga aag ggt aag aaa gtt ctt atc gta gaa Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu 35 40 45	144
cgt gac tgg gct atg cct gat aga att gtt ggt gaa ttg atg caa cca Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro 50 55 60	192
ggg ggt gtt aga gca ttg aga agt ctg ggt atg att caa tct atc aac Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn 65 70 75 80	240
aac atc gaa gca tat cct gtt acc ggt tat acc gtc ttt ttc aac ggc Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly 85 90 95	288
gaa caa gtt gat att cca tac cct tac aag gcc gat atc cct aaa gtt Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val 100 105 110	336
gaa aaa ttg aag gac ttg gtc aaa gat ggt aat gac aag gtc ttg gaa Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu 115 120 125	384
gac agc act att cac atc aag gat tac gaa gat gat gaa aga gaa agg Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg 130 135 140	432
ggg gtt gct ttt gtt cat ggt aga ttc ttg aac aac ttg aga aac att Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile 145 150 155 160	480
act gct caa gag cca aat gtt act aga gtg caa ggt aac tgt att gag Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu 165 170 175	528
ata ttg aag gat gaa aag aat gag gtt gtt ggt gcc aag gtt gac att Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile 180 185 190	576
gat ggc cgt ggc aag gtg gaa ttc aaa gcc cac ttg aca ttt atc tgt Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys 195 200 205	624
gac ggt atc ttt tca cgt ttc aga aag gaa ttg cac cca gac cat gtt Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val 210 215 220	672
cca act gtc ggt tct tcg ttt gtc ggt atg tct ttg ttc aat gct aag Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys 225 230 235 240	720
aat cct gct cct atg cac ggt cac gtt att ctt ggt agt gat cat atg Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met 245 250 255	768

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Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys	
260 265 270	
gct tac aac tct cca aag gtc cca gct gat atc aag agt tgg atg att	864
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile	
275 280 285	
aag gat gtc caa cct ttc att cca aag agt cta cgt cct tca ttt gat	912
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp	
290 295 300	
gaa gcc gtc agc caa ggt aaa ttt aga gct atg cca aac tcc tac ttg	960
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu	
305 310 315 320	
cca gct aga caa aac gac gtc act ggt atg tgt gtt atc ggt gac gct	1008
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala	
325 330 335	
cta aat atg aga cat cca ttg act ggt ggt ggt atg act gtc ggt ttg	1056
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu	
340 345 350	
cat gat gtt gtc ttg ttg att aag aaa ata ggt gac cta gac ttc agc	1104
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser	
355 360 365	
gac cgt gaa aag gtt ttg gat gaa tta cta gac tac cat ttc gaa aga	1152
Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg	
370 375 380	
aag agt tac gat tcc gtt att aac gtt ttg tca gtg gct ttg tat tct	1200
Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser	
385 390 395 400	
ttg ttc gct gct gac agc gat aac ttg aag gca tta caa aaa ggt tgt	1248
Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys	
405 410 415	
ttc aaa tat ttc caa aga ggt ggc gat tgt gtc aac aaa ccc gtt gaa	1296
Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu	
420 425 430	
ttt ctg tct ggt gtc ttg cca aag cct ttg caa ttg acc agg gtt ttc	1344
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe	
435 440 445	
ttc gct gtc gct ttt tac acc att tac ttg aac atg gaa gaa cgt ggt	1392
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly	
450 455 460	
ttc ttg gga tta cca atg gct tta ttg gaa ggt att atg att ttg atc	1440
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile	
465 470 475 480	
aca gct att aga gta ttc acc cca ttt ttg ttt ggt gag ttg att ggt	1488

Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly  
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taa

1491

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 <212> PRT  
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Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys  
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Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu  
 35 40 45

Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro  
 50 55 60

Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn  
 65 70 75 80

Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly  
 85 90 95

Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val  
 100 105 110

Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu  
 115 120 125

Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg  
 130 135 140

Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile  
 145 150 155 160

Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu  
 165 170 175

Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile  
 180 185 190

Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys  
 195 200 205

Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val  
 210 215 220

Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys  
 225 230 235 240

Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met  
 245 250 255

Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys  
 260 265 270

Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile  
 275 280 285

Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp  
 290 295 300

Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu  
 305 310 315 320

Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala  
 325 330 335

Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu  
 340 345 350

His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser  
 355 360 365

Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg  
 370 375 380

Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser  
 385 390 395 400

Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys

	405		410		415
Phe Lys Tyr	Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu				
	420		425		430
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe					
	435		440		445
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly					
	450		455		460
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile					
	465		470		475
					480
Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly					
	485		490		495

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gct ttg aag ctg aag ttt tgc aga aca ccg cta ttc tcc atc tat gat	96
Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp	
20 25 30	
cag tcc acg tct cca tat ctc ttg cac tgt ttc gaa ctg ttg aac ttg	144
Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu	
35 40 45	
acc tcc aga tcg ttt gct gct gtg atc aga gag ctg cat cca gaa ttg	192
Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu	
50 55 60	
aga aac tgt gtt act ctc ttt tat ttg att tta agg gct ttg gat acc	240
Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr	
65 70 75 80	
atc gaa gac gat atg tcc atc gaa cac gat ttg aaa att gac ttg ttg	288
Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu	
85 90 95	

cgt cac ttc cac gag aaa ttg ttg tta act aaa tgg agt ttc gac gga Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly 100 105 110	336
aat gcc ccc gat gtg aag gac aga gcc gtt ttg aca gat ttc gaa tcg Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser 115 120 125	384
att ctt att gaa ttc cac aaa ttg aaa cca gaa tat caa gaa gtc atc Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile 130 135 140	432
aag gag atc acc gag aaa atg ggt aat ggt atg gcc gac tac atc tta Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu 145 150 155 160	480
gat gaa aat tac aac ttg aat ggg ttg caa acc gtc cac gac tac gac Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp 165 170 175	528
gtg tac tgt cac tac gta gct ggt ttg gtc ggt gat ggt ttg acc cgt Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg 180 185 190	576
ttg att gtc att gcc aag ttt gcc aac gaa tct ttg tat tct aat gag Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu 195 200 205	624
caa ttg tat gaa agc atg ggt ctt ttc cta caa aaa acc aac atc atc Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile 210 215 220	672
aga gat tac aat gaa gat ttg gtc gat ggt aga tcc ttc tgg ccc aag Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys 225 230 235 240	720
gaa atc tgg tca caa tac gct cct cag ttg aag gac ttc atg aaa cct Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro 245 250 255	768
gaa aac gaa caa ctg ggg ttg gac tgt ata aac cac ctc gtc tta aac Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn 260 265 270	816
gca ttg agt cat gtt atc gat gtg ttg act tat ttg gcc ggt atc cac Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His 275 280 285	864
gag caa tcc act ttc caa ttt tgt gcc att ccc caa gtt atg gcc att Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile 290 295 300	912
gca acc ttg gct ttg gta ttc aac aac cgt gaa gtg cta cat ggc aat Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn 305 310 315 320	960
gta aag att cgt aag ggt act acc tgc tat tta att ttg aaa tca agg	1008

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg  
 325 330 335

act ttg cgt ggc tgt gtc gag att ttt gac tat tac tta cgt gat atc 1056  
 Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile  
 340 345 350

aaa tct aaa ttg gct gtg caa gat cca aat ttc tta aaa ttg aac att 1104  
 Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile  
 355 360 365

caa atc tcc aag atc gaa cag ttt atg gaa gaa atg tac cag gat aaa 1152  
 Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys  
 370 375 380

tta cct cct aac gtg aag cca aat gaa act cca att ttc ttg aaa gtt 1200  
 Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val  
 385 390 395 400

aaa gaa aga tcc aga tac gat gat gaa ttg gtt cca acc caa caa gaa 1248  
 Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu  
 405 410 415

gaa gag tac aag ttc aat atg gtt tta tct atc atc ttg tcc gtt ctt 1296  
 Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu  
 420 425 430

ctt ggg ttt tat tat ata tac act tta cac aga gcg tga 1335  
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 435 440

<210> 10  
 <211> 444  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 10

Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Val Glu Met Lys Ala  
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Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp  
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Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu  
 35 40 45

Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu  
 50 55 60

Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr  
 65 70 75 80

Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu  
85 90 95

Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly  
100 105 110

Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser  
115 120 125

Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile  
130 135 140

Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu  
145 150 155 160

Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp  
165 170 175

Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg  
180 185 190

Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu  
195 200 205

Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile  
210 215 220

Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys  
225 230 235 240

Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro  
245 250 255

Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn  
260 265 270

Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His  
275 280 285

Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile  
290 295 300



Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn  
 305 310 315 320

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg  
 325 330 335

Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile  
 340 345 350

Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile  
 355 360 365

Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys  
 370 375 380

Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val  
 385 390 395 400

Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu  
 405 410 415

Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu  
 420 425 430

Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala  
 435 440

<210> 11  
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 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of synthetic sequence: AtHT-5'

<220>  
 <221> misc\_feature  
 <222> (1)..(35)  
 <223> Primer

<400> 11  
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35

<210> 12

<211> 32  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of synthetic sequence: AtHT-3'

<220>  
 <221> misc\_feature  
 <222> (1)..(32)  
 <223> Primer

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 aactcgagag acacatggtg ctgttggtgct tc

32

<210> 13  
 <211> 60  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of synthetic sequence: ERG5-Crelox-5'

<220>  
 <221> misc\_feature  
 <222> (1)..(60)  
 <223> Primer

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60

<210> 14  
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60

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62